

FIG. 1

HSP 90-beta (Mouse)
SEQ ID NO:1

```

1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasa ldkiryeslt
61 dpskldsgke lkidiipnpq ertlt1vdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddeqyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vkkhhsqfig ypitlyleke rekeisdeea eeekgekeeee
241 dkdddeekpki edvgsdeedd sgdkdkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefyksltm dwdhlavkh fsvegglefr allfiprap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremlqgqski lkvirknivk kcelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgfev vymtepiday cvqqlkefdg kslvsvtkeg
541 lelpedeeek kkmeeeskafk enlcklmkei ldkkvekvti snrlvssspcc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vndlvvllfe
661 tallssgfs1 edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 90-beta (Human)
SEQ ID NO:2

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1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasa ldkiryeslt
61 dpskldsgke lkidiipnpq ertlt1vdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddeqyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vkkhhsqfig ypitlyleke rekeisdeea eeekgekeeee
241 dkdddeekpki edvgsdeedd sgdkdkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefyksltm dwdhlavkh fsvegglefr allfiprap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremlqgqski lkvirknivk kcelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgfev vymtepiday cvqqlkefdg kslvsvtkeg
541 lelpedeeek kkmeeeskafk enlcklmkei ldkkvekvti snrlvssspcc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vndlvvllfe
661 tallssgfs1 edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 90-alpha (Human)
SEQ ID NO:3

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1 mpeetqtqdq pmeeeeevetf afqaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhnl ipnkqdrllt ivdtgigmkt adlinnlgti aksgtkafme
121 alqagadism igqfgvfgys aylvaekvtv itkhnddeq awessaggsf tvrttgtgem
181 grgtkvilhl kedqteylee rrikeivkhh sqfigypitl fvekerdkev sddeaeeked
241 keeekekeek esedkpeied vgsdeeeeekk dgdkkkkkki kekyidqeel nktkpiwtrn
301 pdditneeyg efykslndw edhlavkhfs veggglefral lfvpprapfd lfenrkkkmn
361 iklyvrrvfi mdncestlpe ylnfirgvvd sedlplnisr emlqgqskilk virknlvkkc
421 lelf telaed kenykkfyeq fskmikligh edsqrkksl ellryytsas gdemvslkd
481 ctrmkengkh iyyitgetkd qvansafver lrkhgleviy miepideycv qqlkefegkt
541 lvsvtkegle lpedeeekkk geekktkfen lckimkdlie kkvekvvvsn rlvtsppciv
601 tstygwtanm erimkaqalr dnstmgymaa kkhleinpdh sietlrqka eadkndksvk
661 dlvillyeta llssgfsled pqthanriyr miklglgide ddptaddtsa avteempple
721 gdddttsrmee vd

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HSP 84 (Mouse)
SEQ ID NO:4

1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpszldsgke 1kidiipnpq ertltlvdgt igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddeqyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkkhsqfig ypitlyleke rekeisdeea eeekgekeeee
241 dkdedekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefyksltn dwedhlavkh fsveggglefr allfiprrap fdifenkdkk nniklyvrrv
361 fidmcdeli peylnfirgv vdsedlplni sremlqgqski lkvirknivk kcelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgfev vymtepidey cvqqlkefdg kslvsvtkeg
541 lelpedeekk kkmeeeskakf enlcklmkei ldkkvekvti snrlvssspcc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeakndka vndlvvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevtaeep saavpdeipp legdedasrm
721 eevd

HSP 84 (Human)
SEQ ID NO:5

1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpszldsgke 1kidiipnpq ertltlvdgt igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddeqyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkkhsqfig ypitlyleke rekeisdeea eeekgekeeee
241 dkdedekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefyksltn dwedhlavkh fsveggglefr allfiprrap fdifenkdkk nniklyvrrv
361 fidmcdeli peylnfirgv vdsedlplni sremlqgqski lkvirknivk kcelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgfev vymtepidey cvqqlkefdg kslvsvtkeg
541 lelpedeekk kkmeeeskakf enlcklmkei ldkkvekvti snrlvssspcc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeakndka vndlvvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

HSP 86 (Mouse)
SEQ ID NO:6

1 mpeetqtqdq pmeeeeevetf afqaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhnl ipskqdrllt ivdtgigmtk adlinnlgti aksgtkafme
121 algagadism igqfgvgfys aylvaekvttv itkhnddeqy awessaggst tvrtdtgepm
181 grgtkvihl kedqteylee rrikeivkkh sqfigypitl fvekerdkev sddeaeek
241 keeekekek esddkpeied vgsdeeeeek kdgdkkkkk ikekyidqe elnktkpiwtr
301 npdditneey gefykslnd weehlavkhf sveggglefra llfprrapf dlfenrkkkn
361 niklyvrrvf imdnceelip eylnfirgvv dsedlplnis remlqgqskil kvirknlvkk
421 clelfelae dkenykkfy qfskniklgi hedsqnrkk1 sellryytsa sgdemvslkd
481 yctrmkengk hiyfitgetk dqvansafve rlrkhglevi ymiedepidey vqqlkefegk
541 tlvsvtkegl elpedeeekk kgeekktkfe nlckimkdl ekkvekvvs nrlvtspcc
601 vtstygtan merimkaqal rdnstmgyma akkhleinpd hsietlrqk aeadkndksv
661 kdlvvlyet allssgfsle dpqthanriy rmiklglgid eddptvddts aavteemppl
721 egdddttsrme evd

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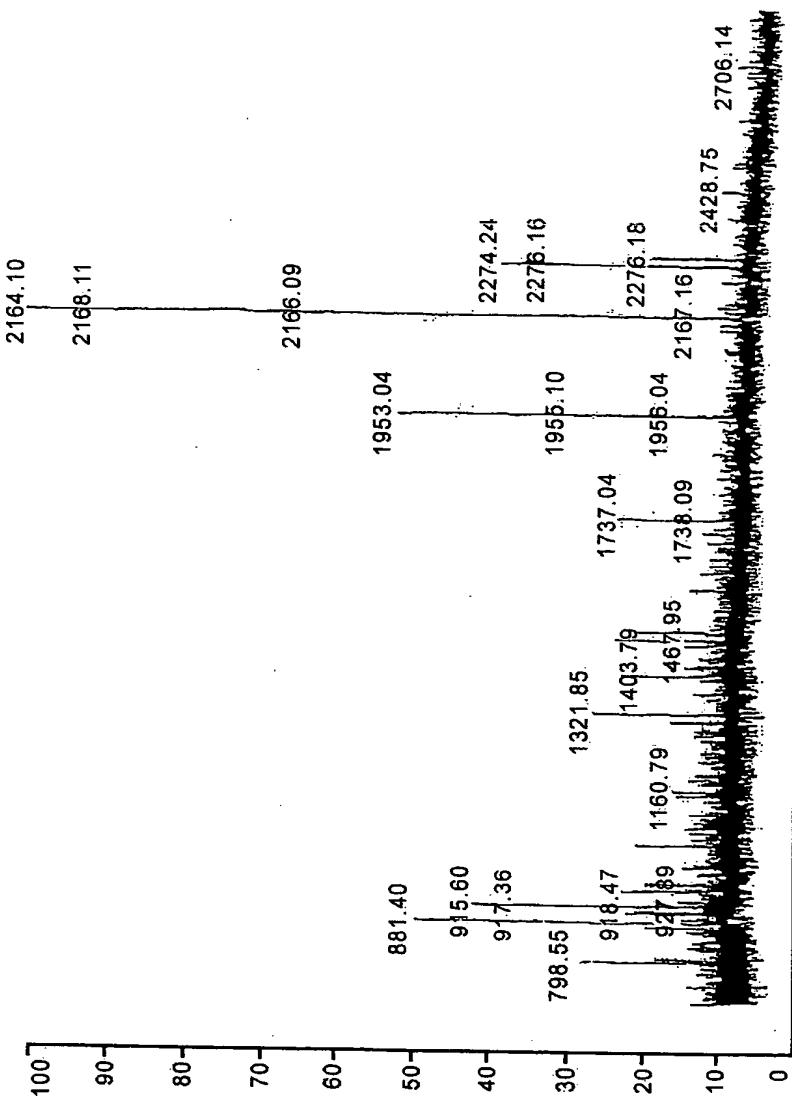


FIG. 10

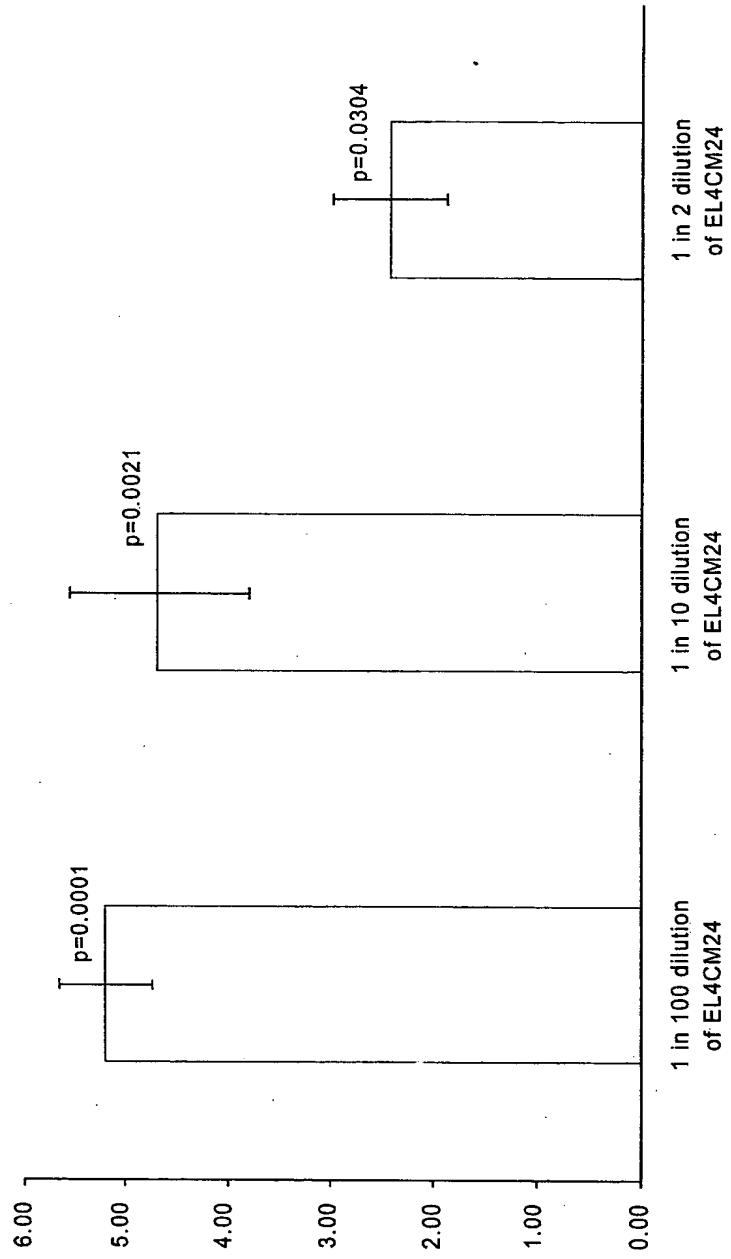
HSP 86, HSP 60 (Human)
SEQ ID NO:7

1 mlrlptvfrq mwpvsivlap hltrayakdv kfgadaralm lggvdllada vavtmgpkr
61 tvieqswgs pkvtdkgvtv aksidlkdky knigaklvqd vanntneeag dgtttatvla
121 rsiakegfe kskganpvei rrgvmlavda viaelkkqsk pvtpeeiaq vatisangdk
181 eignisdam kkvgrokvit vkgktlnde leiegmkfd rgyispyfin tskgqkcefq
241 dayvlsekk issiqsiypa leianahrkp lviaeavdg ealstlavl nr lkvgllqvav
301 kapgfgdnrk nqlkdmaiat ggavfgeegl tlnledvqph dlkgvgeviv tkddamlikg
361 kgdkaqiekr iqeiiieqldv ttseyekel nerlaklsdg vavlkvggts dvevnekkdir
421 vtdalnatra aveegivlgg gcallrcipa ldsltpaned qkigieikr tlkipamtia
481 knagvegsli vekimqssse vgydamagdf vnmvekgiid ptkvvrtall daagvasllt
541 taevvvteip keekdpgmga mggmgggm gg maf

L-plastin (Human)
SEQ ID NO:8

1 margsvsdee mmelreafak vdtdgngyis fnelndlfka aclplpgyrv reitenlmat
61 gdldqdgri fdefikifhg lkstdvaktf rkainkkegi caiggtseqs svgtqhsyse
121 eekyafvnwi nkalendpdc rhvipmnpnt ndlfnavgdg ivlckminls vpdtiderti
181 nkkkltpfti qenlnlalns asaigchvvn igaedlkegk pylvlgllwq vikiglfadi
241 elsrnealia llregesled lmklsppeell lrwanyhlen agcnkignfs tdikdskayy
301 hllegqvapkg deegvpavvi dmsglrekdd iqraecmlqq aerlgcrqfv tatdvrgnp
361 klnlafianl fnrypalhkp enqdidwgal egetreertf rnwmmslgnv prvnhlysd
421 sdalvifqly ekikvpvdwn rvnkppypk1 ggnmkklenc nyavelgknq akfslvgigg
481 qdlnegnrtl tlaliwqlmr rytnileei gggqkvnddi ivnwvnetlr eaeckssiss
541 fkdpkistsl pvlldlidaiq pgsinydlk tenlnddekl nnakyaisma rkigarvyal
601 pedlvevnpk mvmtvfaclm gkgmkrv

FIG. 2
EL4 Conditioned Media Repels T cell *in vitro*



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FIG. 3
Heat Inactivation and Proteinase K Digestion of EL4CM24

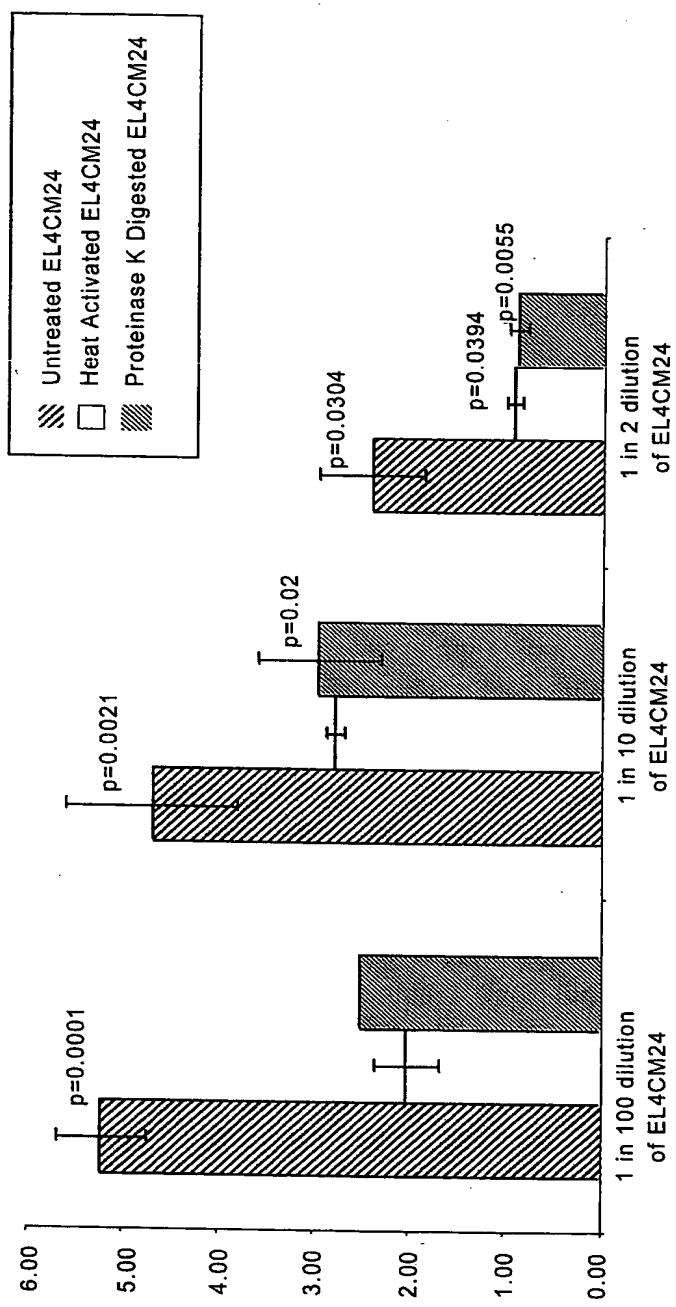
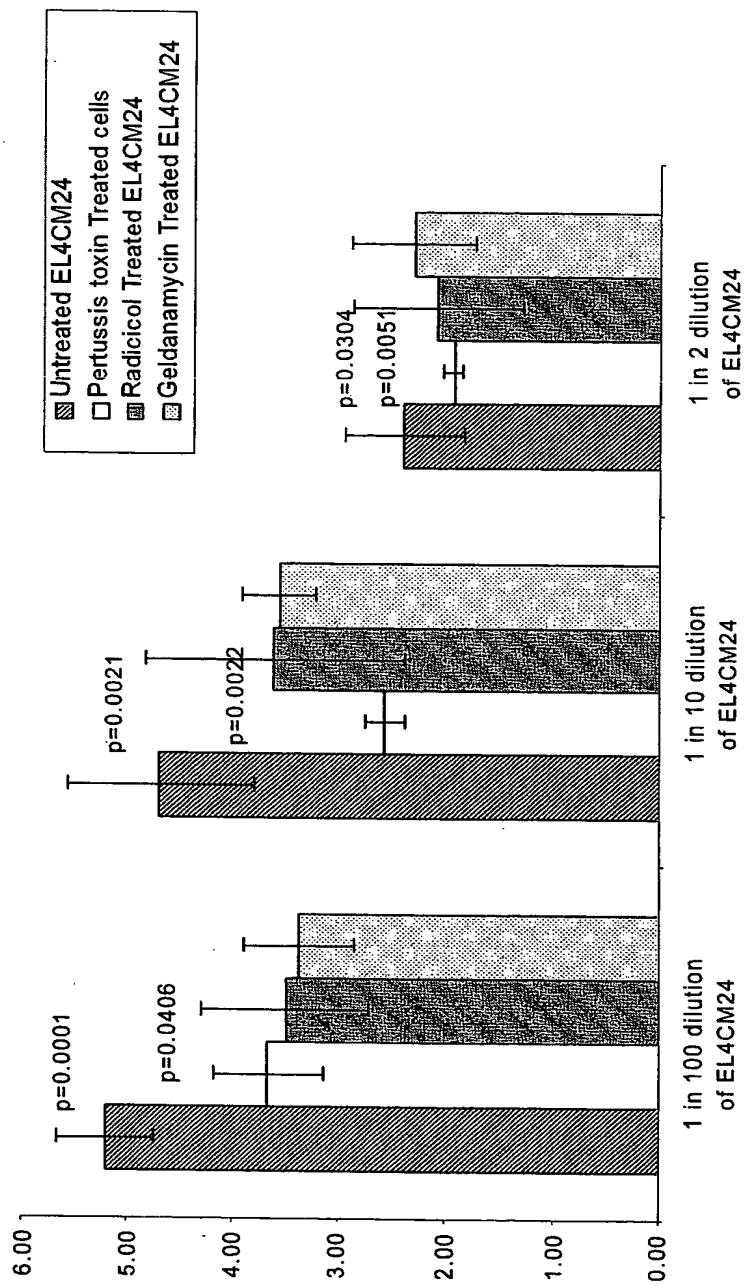
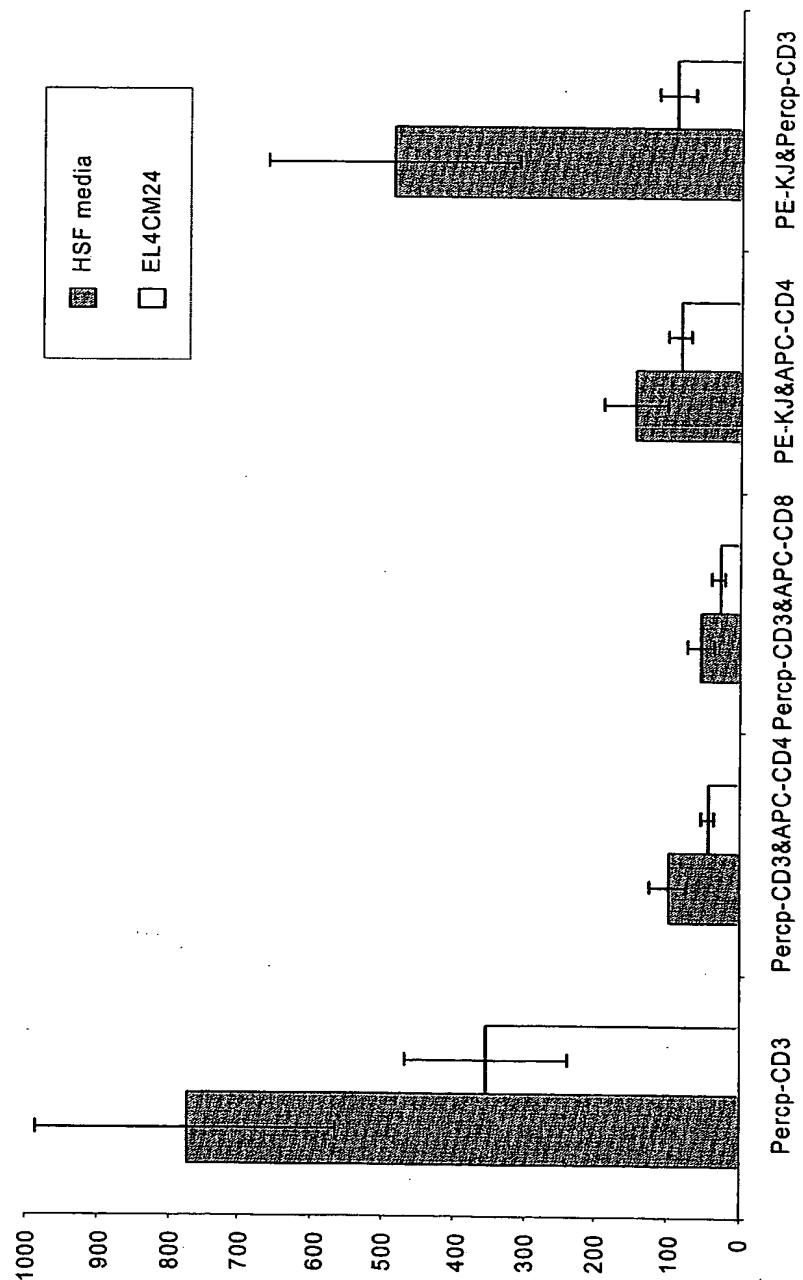


FIG. 4
Use of Specific Inhibitors



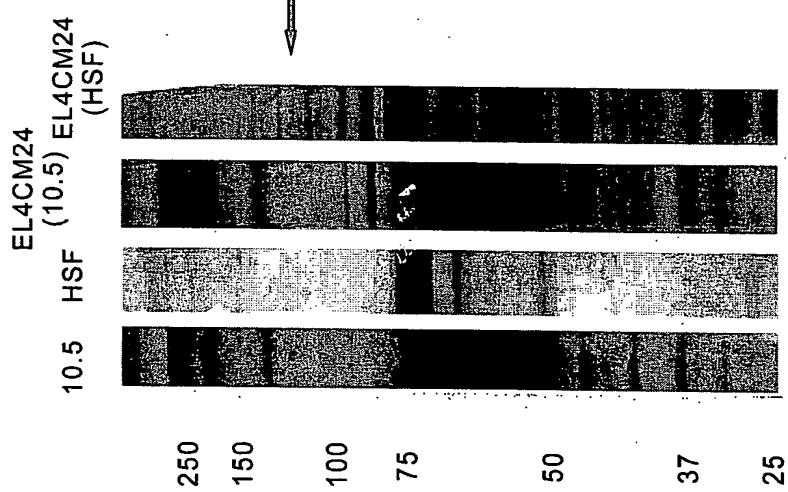
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FIG. 5
EL4 Conditioned Media Repels T cells *in vivo*



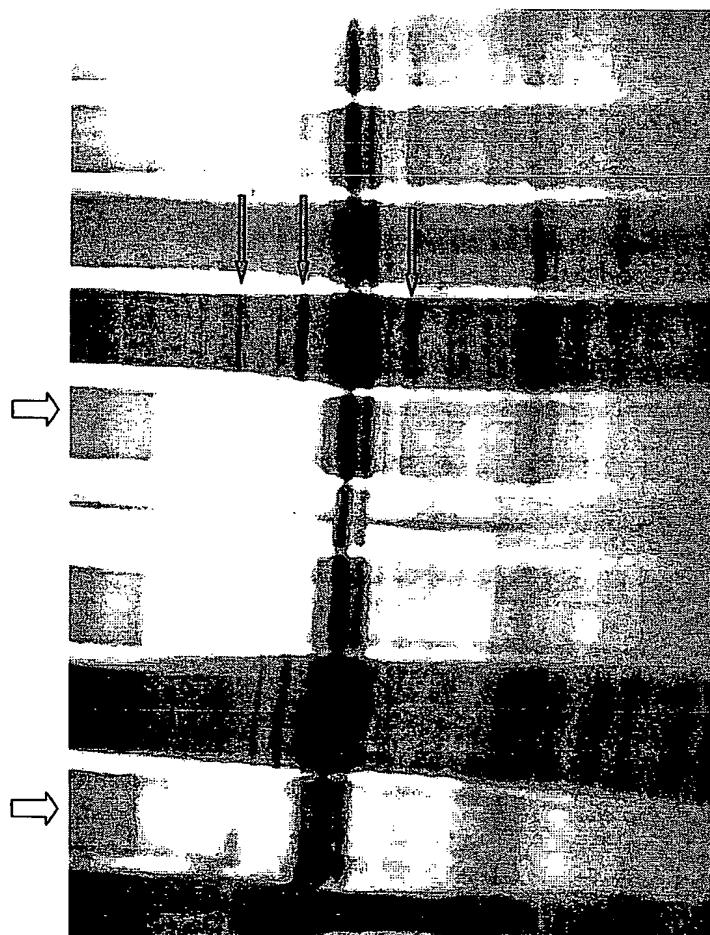
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FIG. 6
EL4CM24 SDS PAGE



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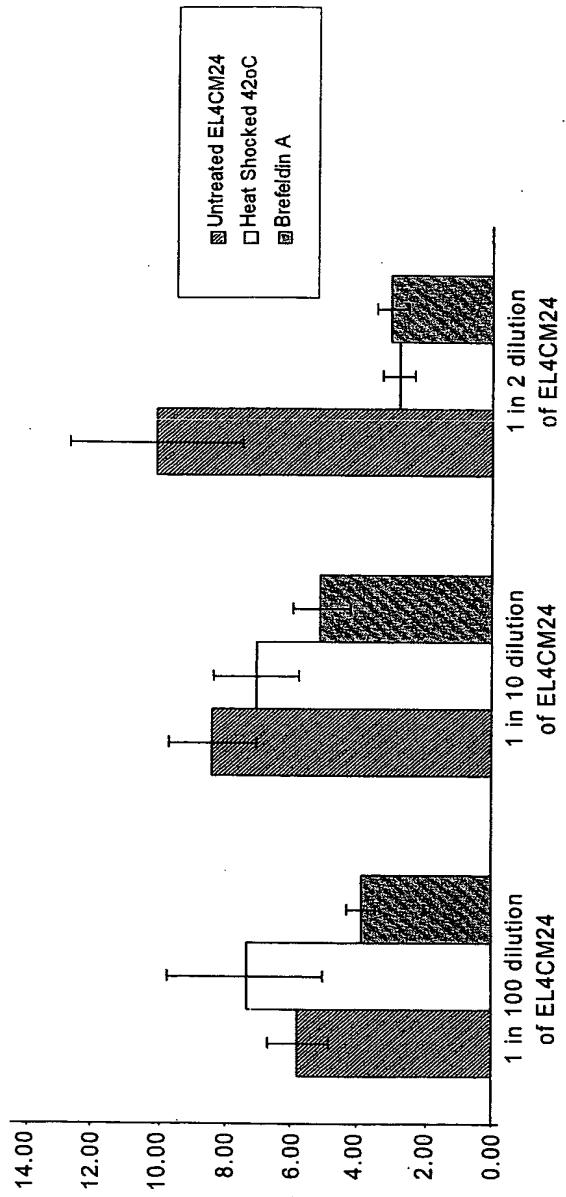
FIG. 7
Ion Exchange Chromatography



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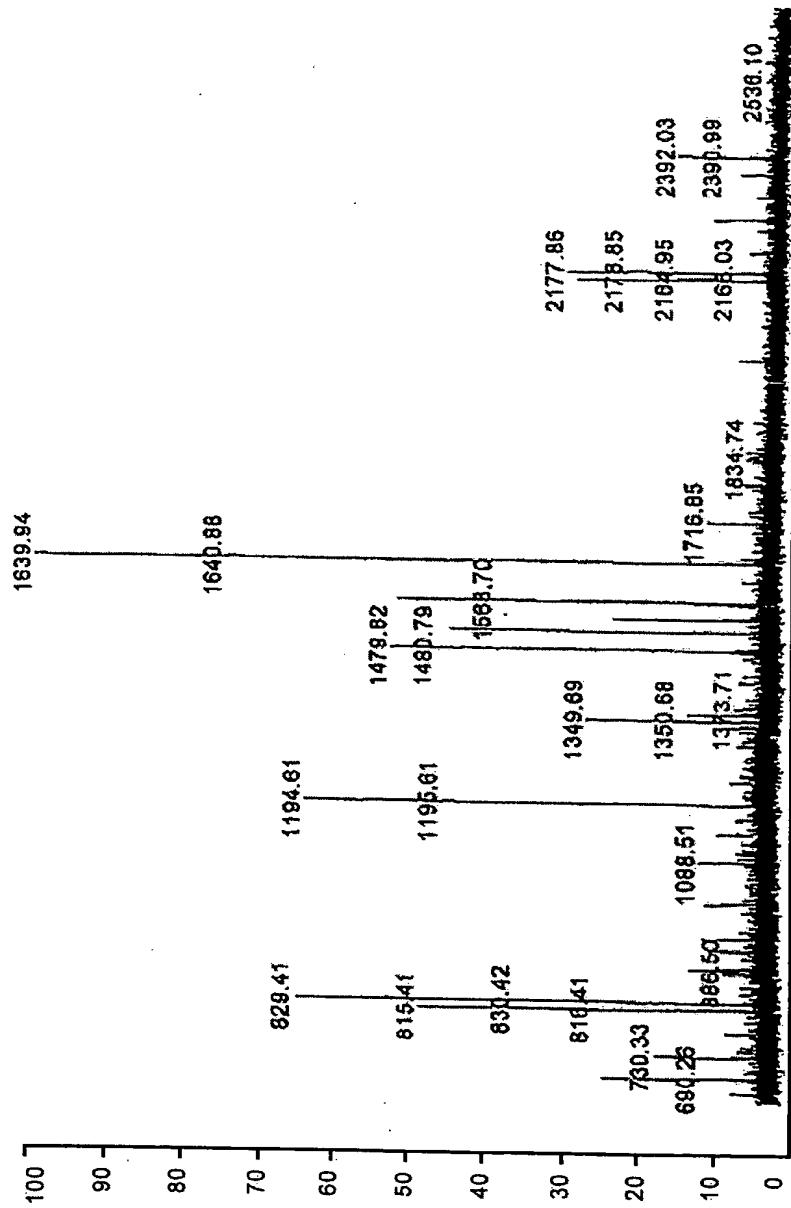
FIG. 8

Heat Shock of EL4 @ 42°C and Brefeldin A treatment of EL4



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FIG. 9



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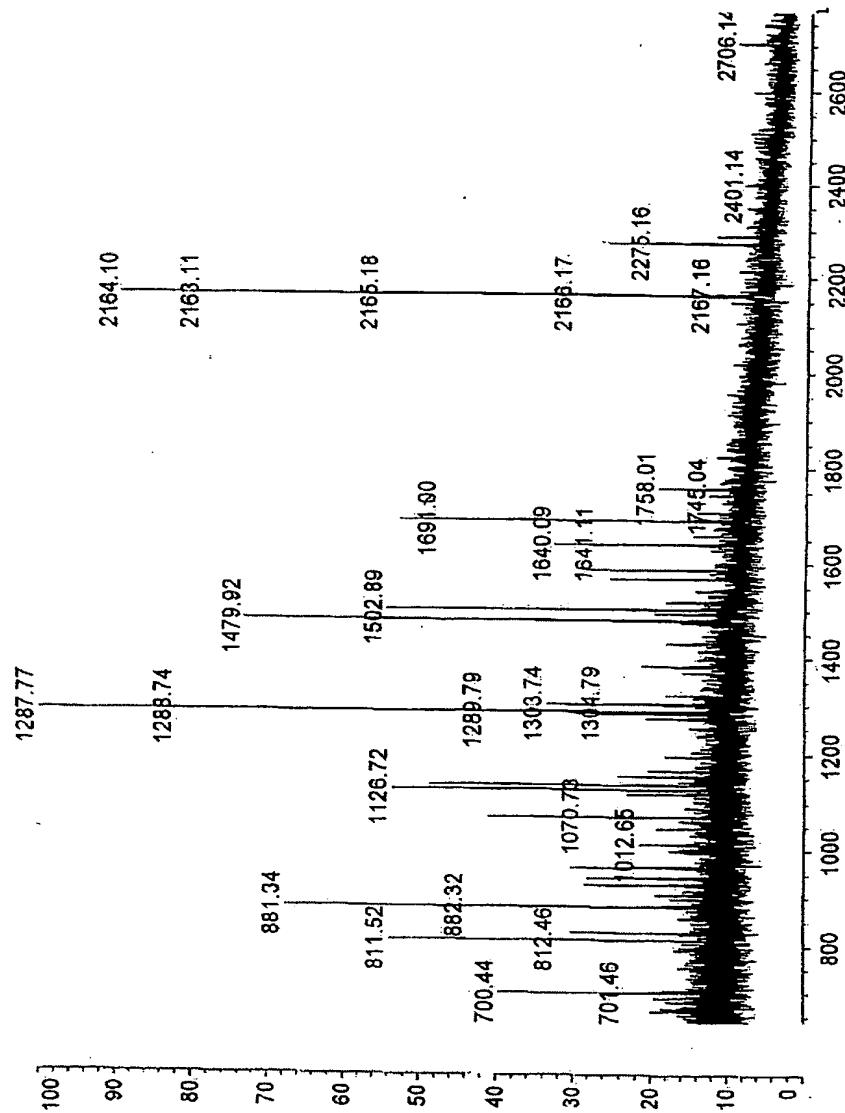


FIG. 12A

MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest

Databasc searched: NCBInr.121002

Molecular weight search (1000 - 100000 Da) selects 1195692 entries.

Full pI range: 1247039 entries.

Species search (MAMMALS) selects 197947 entries.

Combined molecular weight, pI and species searches select 186900 entries.

MS-Fit search selects 407 entries (results displayed for top 4 matches).

Considered modifications: | Peptide N-terminal Gln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Peptide										Input #
Min. #	Mass	Peptide	Digest	Max. #	Cysteines	Peptide	Peptide	Peptide	Peptide	
Peptides	Tolerance	Masses	Used	Missed	Modified	N terminus	C terminus	Free Acid (O H)	Peptide Masses	
to Match	(+/-)	are	Trypsin	Cleavages	by	Hydrogen (H)				15
4	150.000	monoisotopic		1	acrylamide					
	ppm									

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBInr.121002 Accession #	Protein Name
1	7.02e+003	8/15 (53%)	81963.2 / 4.99	EQUUS CABALLUS	<u>20177936</u>	heat shock protein 90 beta
2	6.91e+003	8/15 (53%)	83264.6 / 4.97	HOMO SAPIENS	<u>20149594</u>	Unknown (protein for MGC:1138)
3	5.79e+003	8/15 (53%)	84843.9 / 5.26	HOMO SAPIENS	<u>11277141</u>	hypothetical protein
4	2.25e+003	7/15 (46%)	83316.8 / 5.06	RATTUS SP.	<u>1346320</u>	heat shock protein 90; hsp90

Detailed Results

1. 8/15 matches (53%). 81963.2 Da, pI = 4.99. Acc. # 20177936. EQUUS CABALLUS. heat shock protein 90 beta .

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	570	575	(K)V TISNR(L)	
829.4100	829.5300	-144.6415	323	329	(R)ALL FIPR(R)	
891.3500	891.4252	-84.4094	421	427	(K)F YEAFSK(N)	
1194.6100	1194.6483	-32.0277	65	74	(K)D IIPNPQER(T)	
1348.6900	1348.6650	18.5557	312	322	(K)H FSVEGOLEFR(A)	
1513.7800	1513.7862	-4.1036	371	384	(R)G VVDSEDLPLNISR(E)	
2176.8600	2176.9457	-39.3681	449	467	(R)Y HTSOSGDEMITSLEYVSR(M)	
2390.9900	2391.1832	-80.8096	474	494	(K)S IYYITGESKEQVANSAFVER(V)	

7 unmatche masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (95/713 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 120570

FIG. 12B

2. 8/15 matches (53%). 83264.6 Da, pI = 4.97. Acc. # 20149594. HOMO SAPIENS. Unknown (protein for MGC:1138).

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	578	583	(K)Y T ISNR(L)	
829.4100	829.5300	-144.6415	331	337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429	435	(K)FYEA F SK(N)	
1194.6100	1194.6483	-32.0277	73	82	(K)ID I LPNPOER(T)	
1348.6900	1348.6650	18.5557	320	330	(K)HES V E G OLEFR(A)	
1513.7800	1513.7862	-4.1036	379	392	(R)GV V DSE D LPLNISR(E)	
2176.8600	2176.9457	-39.3681	457	475	(R)YHT S OSGDEM T SLSEY V SR(M)	
2390.9900	2391.1832	-80.8096	482	502	(K)SIYYITGESK E OVANSA F YER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (95/724 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): [137455](#)

3. 8/15 matches (53%). 84843.9 Da, pI = 5.26. Acc. # 11277141. HOMO SAPIENS. hypothetical protein.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	578	583	(K)Y T ISNR(L)	
829.4100	829.5300	-144.6415	331	337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429	435	(K)FYEA F SK(N)	
1194.6100	1194.6483	-32.0277	73	82	(K)ID I LPNPOER(T)	
1348.6900	1348.6650	18.5557	320	330	(K)HES V E G OLEFR(A)	
1513.7800	1513.7862	-4.1036	379	392	(R)GV V DSE D LPLNISR(E)	
2176.8600	2176.9457	-39.3681	457	475	(R)YHT S OSGDEM T SLSEY V SR(M)	
2390.9900	2391.1832	-80.8096	482	502	(K)SIYYITGESK E OVANSA F YER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 12% (95/737 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): [1101236](#)

4. 7/15 matches (46%). 83316.8 Da, pI = 5.06. Acc. # 1346320. RATTUS SP.. heat shock protein 90: hsp90.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	578	583	(K)Y T ISNR(L)	
829.4100	829.5300	-144.6415	331	337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429	435	(K)FYEA F SK(N)	
1348.6900	1348.6650	18.5557	320	330	(K)HES V E G OLEFR(A)	
1513.7800	1513.7862	-4.1036	379	392	(R)GV V DSE D LPLNISR(E)	
2176.8600	2176.9457	-39.3681	457	475	(R)YHT S OSGDEM T SLSEY V SR(M)	
2390.9900	2391.1832	-80.8096	482	502	(K)SIYYITGESK E OVANSA F YER(V)	

8 unmatched masses: 730.3300 815.4100 1194.6100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely.

Sample ID (comment): Apo A-1 1040 AKPVLEDLR

Database searched: NCBI nr.121002

Full Molecular Weight range: 1247039 entries.

Full pI range: 1247039 entries.

Species search (MAMMALS) selects 197947 entries.

Number of sequences passing through parent mass filter: 4253

MS-Tag search selects 7 entries (results displayed for top 3 matches).

Parent mass: 1194.6100 (+/- 0.2000 Da)

Fragment Ions used in search: 175.31, 212.00, 229.20, 342.62, 355.43, 512.43, 529.50, 626.31, 713.44, 740.58, 966.73 (+/- 0.50 Da)

Ion Types Considered: a b B y o b I

Search Mode	Max. # Unmatched ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus	Peptide C terminus
Identity	1		Trypsin	1		Hydrogen (H)	Free Acid (O H)

Result Summary

Rank	# Unmatched ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	Protein Name
1	0/11	(K)ID I LPNPOER(T)	1194.6483	-0.0383	83325.7 / 4.97	MOUSE	123681	Heat shock protein HSP 90-beta (HSP 84) (Tumor specific transplantation 84 kDa antigen) (TSTA)
1	0/11	(K)ID I LPNPOER(T)	1194.6483	-0.0383	83361.1 / 5.03	MUS MUSCULUS	6680305	heat shock protein, 84 kDa 1
1	0/11	(K)ID I LPNPOER(T)	1194.6483	-0.0383	14066.4 / 4.64	HOMO SAPIENS	2351110	heat shock protein beta

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FIG. 12C

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBIInr.121002 Accession #	MS-Digest Index #	Protein Name				
1	0/11	(K)DILPNPQER(T)	1194.6483	-0.0383	83325.7 / 4.97	MOUSE	<u>123681</u>	<u>318176</u>	heat shock protein HSP 90-beta (HSP 84) (Tumor specific transplantation 84 kDa antigen) (TSTA)				
1	0/11	(K)DILPNPQER(T)	1194.6483	-0.0383	83361.1 / 5.03	MUS MUSCULUS	<u>6680305</u>	<u>583998</u>	heat shock protein, 84 kDa 1				
Fragment-ion (m/z) 175.31 212.00 229.20 342.62 355.43 512.43 529.50 626.31 723.44 740.58 966.73													
		Ion-type Delta Da	y ₁ 0.19	NP -0.10	b ₂ 0.08	b ₃ 0.42	PQE 0.27	y ₄ -NH ₃ 0.18	y ₄ 0.23	y ₅ -NH ₃ 0.02	y ₆ -NH ₃ 0.10	y ₆ 0.21	y ₈ 0.19
1	0/11	(K)DILPNPQER(T)	1194.6483	-0.0383	14066.4 / 4.64	HOMO SAPIENS	<u>2351110</u>	<u>587097</u>	heat shock protein beta				
		Ion-type Delta Da	y ₁ 0.19	NP -0.10	b ₂ 0.08	b ₃ 0.42	PQE 0.27	y ₄ -NH ₃ 0.18	y ₄ 0.23	y ₅ -NH ₃ 0.02	y ₆ -NH ₃ 0.10	y ₆ 0.21	y ₈ 0.19

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely.

Sample ID (comment): Apo A-1 1040 AKPVLEDLR

Database searched: NCBIInr.121002

Molecular weight search (1000 - 100000 Da) selects 1195692 entries.

Full pI range: 1247039 entries.

Species search (MAMMALS) selects 197947 entries.

Combined molecular weight, pI and species searches select 186900 entries.

Number of sequences passing through parent mass filter: 4989

MS-Tag search selects 18 entries (results displayed for top 3 matches).

Parent mass: 815.4100 (+/- 0.2000 Da)

Fragment Ions used in search: 185.26, 255.27, 272.34, 298.32, 354.45, 371.53, 417.39, 445.25, 518.35 (+/- 0.50 Da)

Ion Types Considered: a b y n h I

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by	Peptide N terminus	Peptide C terminus
identity	1		Trypsin	1	acrylamide	Hydrogen (H)	Free Acid (O H)

Result Summary

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBIInr.121002 Accession #	Protein Name
1	0/9	(R)ALLFVPR(R)	815.5143	-0.1043	75541.0 / 5.28	MUS MUSCULUS	<u>20882565</u>	similar to heat shock protein 86
1	0/9	(R)ALLFVPR(R)	815.5143	-0.1043	84674.2 / 4.94	HOMO SAPIENS	<u>123678</u>	90 kDa heat-shock protein (AA 1-732)
1	0/9	(K)AILFVPR(R)	815.5143	-0.1043	57068.0 / 6.38	HOMO SAPIENS	<u>12804541</u>	hypothetical protein LOC63929

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBIInr.121002 Accession #	MS-Digest Index #	Protein Name		
1	0/9	(R)ALLFVPR(R)	815.5143	-0.1043	75541.0 / 5.28	MUS MUSCULUS	<u>20882565</u>	<u>615811</u>	similar to heat shock protein 86		
1	0/9	(R)ALLFVPR(R)	815.5143	-0.1043	84674.2 / 4.94	HOMO SAPIENS	<u>123678</u>	<u>162860</u>	90 kDa heat-shock protein (AA 1-732)		
Fragment-ion (m/z) 185.26 255.27 272.34 298.32 354.45 371.53 417.39 445.25 518.35											
		Ion-type Delta Da	b ₂ 0.13	y ₂ -NH ₃ 0.12	y ₂ 0.17	b ₃ 0.11	y ₃ -NH ₃ 0.24	y ₃ 0.29	a ₄ 0.10	d ₄ -0.03	y ₄ 0.04
1	0/9	(K)AILFVPR(R)	815.5143	-0.1043	57068.0 / 6.38	HOMO SAPIENS	<u>12804541</u>	<u>171353</u>	hypothetical protein LOC63929		
		Ion-type Delta Da	b ₂ 0.13	y ₂ -NH ₃ 0.12	y ₂ 0.17	b ₃ 0.11	y ₃ -NH ₃ 0.24	y ₃ 0.29	a ₄ 0.10	d ₄ -0.03	y ₄ 0.04

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FIG. 13A

MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest

Database searched: NCBInr.51403

Molecular weight search (1000 - 200000 Da) selects 1421445 entries.

Full pI range: 1432416 entries.

Species search (HUMAN RODENT) selects 224838 entries.

Combined molecular weight, pI and species searches select 222557 entries.

MS-Fit search selects 5 entries (results displayed for top 3 matches).

Considered modifications: | Peptide N-terminal Gln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-)	Peptide Masses are monoisotopic	Digest Used	Max. # Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)	Input # Peptide Masses
7	150.000 ppm		Trypsin	1				13

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBInr.51403 Accession #	Protein Name
1	1.81e+003	7/13 (53%)	94057.0 / 5.13	RATTUS NORVEGICUS	24025637	ischemia responsive 94 kDa protein
2	449	7/13 (53%)	94081.1 / 5.13	MUS MUSCULUS	13277753	heat shock protein 4
2	449	7/13 (53%)	94133.1 / 5.15	MUS MUSCULUS	6680301	apg-2

Detailed Results

1. 7/13 matches (53%). 94057.0 Da, pI = 5.13. Acc. # 24025637. RATTUS NORVEGICUS. ischemia responsive 94 kDa protein.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
798.5500	798.4514	123.4893	431	436	(K)VLT F YR(K)	
949.6100	949.5219	92.7425	62	69	(K)NTVQGF K R(F)	
1321.8500	1321.7116	104.7200	222	234	(K)VIA T A F D T TLGG R (K)	
1402.7800	1402.6313	106.0213	619	629	(K)NA V E Y Y V EMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGGIETIANEYS D R(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EFSITD V V P Y P ISLR(W)	
1953.0400	1952.8336	105.6759	406	422	(R)WNSPAEGSSDCEV F PK(N)	

6 unmatched masses: 915.6000 917.3600 1305.8400 1478.8800 1587.9500 1624.0500

The matched peptides cover 10% (84/840 AA's) of the protein.
 Coverage Map for This Hit (MS-Digest index #): [787619](#)

2. 7/13 matches (53%). 94081.1 Da, pI = 5.13. Acc. # 13277753. MUS MUSCULUS. heat shock protein 4.

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FIG. 13B

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
798.5500	798.4514	123.4893	431	436	(K)VLTFYR(K)	
949.6100	949.5219	92.7425	62	69	(K)NTVQGFKR(F)	
1305.8400	1305.7418	75.1849	670	680	(K)QVYVVDKLAELK(S)	
1321.8500	1321.7116	104.7200	222	234	(K)VLATAFDTTLGGR(K)	
1402.7800	1402.6313	106.0213	620	630	(K)NAVEEYVYEMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGGIETIANEYSDR(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EFSITDVVVPYPISLR(W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 202745

2. 7/13 matches (53%). 94133.1 Da, pI ~ 5.15. Acc. # 6680301. MUS MUSCULUS. apg-2.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
798.5500	798.4514	123.4893	431	436	(K)VLTFYR(K)	
949.6100	949.5219	92.7425	62	69	(K)NTVQGFKR(F)	
1305.8400	1305.7418	75.1849	670	680	(K)QVYVVDKLAELK(S)	
1321.8500	1321.7116	104.7200	222	234	(K)VLATAFDTTLGGR(K)	
1402.7800	1402.6313	106.0213	620	630	(K)NAVEEYVYEMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGGIETIANEYSDR(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EFSITDVVVPYPISLR(W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 1179227

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FIG. 14A

MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest

Database searched: NCBIInr.51403

Molecular weight search (1000 - 100000 Da) selects 1372760 entries.

Full pI range: 1432416 entries.

Species search (HUMAN RODENT) selects 224838 entries.

Combined molecular weight, pI and species searches select 211465 entries.

MS-Fit search selects 335 entries (results displayed for top 3 matches).

Considered modifications: | Peptide N-terminal Gln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Peptides to Match	Min. #	Peptide Masses	Digest Used	Max. # Missed Cleavages	Cysteines Modified by	Peptide N terminus	Peptide C terminus	Input # Peptide Masses
4	150.000	monoisotopic	Trypsin	1	acrylamide	Hydrogen (H)	Free Acid (O H)	17
	ppm							

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBIInr.51403 Accession #	Protein Name
1	1.22e+005	11/17 (64%)	70149.7 / 5.20	MUS MUSCULUS	<u>29840803</u>	unnamed protein product
2	1.22e+005	11/17 (64%)	70163.8 / 5.24	MUS MUSCULUS	<u>26326929</u>	unnamed protein product
3	2.66e+004	10/17 (58%)	70201.8 / 5.28	MUS MUSCULUS	<u>6679385</u>	65-kDa macrophage protein

Detailed Results

1. 11/17 matches (64%). 70149.7 Da, pI = 5.20. Acc. # 29840803. MUS MUSCULUS. unnamed protein product.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YAISMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)VNKPPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPEELLRLR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFVTATDVVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MNLSPVPTDER(T)	
1585.9400	1585.8477	58.1710	597	610	(R)VYALPEDLVEVNPK(M)	
1689.9700	1689.8560	67.4478	473	488	(K)FSLVGIAQQLNEGNR(T)	
1758.0100	1757.8744	77.1528	310	326	(K)GDFEGIPAVVIDMSCLR(E)	

6 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

The matched peptides cover 19% (120/627 AA's) of the protein.

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FIG. 14B

Coverage Map for This Hit (MS-Digest index #): 372720

2. 11/17 matches (64%). 70163.8 Da, pI = 5.24. Acc. # 26326929. MUS MUSCULUS. unnamed protein product.

submitted	m/z	MH ⁺	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
	700.4400	700.4146	36.2352	77	82	(K)VFFHGLK(S)	
	811.5200	811.4136	131.0872	585	591	(K)YAISMAR(K)	
	942.5800	942.5413	41.0831	442	449	(R)VNKPYPK(L)	
	1069.7200	1069.6257	88.1285	264	272	(K)LSPEELLRLR(W)	
	1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
	1135.7100	1135.6111	87.0474	348	357	(R)QFVTATDVVR(G)	
	1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
	1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDER(T)	
	1585.9400	1585.8477	58.1710	597	610	(R)VYALPEDLVEVNPK(M)	
	1689.9700	1689.8560	67.4478	473	488	(K)FSLVCGIAGODLNEGNR(T)	
	1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVIDMSCLR(E)	

6 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

The matched peptides cover 19% (120/627 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 1174311

3. 10/17 matches (58%). 70201.8 Da, pI = 5.28. Acc. # 6679385. MUS MUSCULUS. 65-kDa macrophage protein.

submitted	m/z	MH ⁺	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
	700.4400	700.4146	36.2352	77	82	(K)VFFHGLK(T)	
	811.5200	811.4136	131.0872	585	591	(K)YAISMAR(K)	
	942.5800	942.5413	41.0831	442	449	(R)VNKPYPK(L)	
	1069.7200	1069.6257	88.1285	264	272	(K)LSPEELLRLR(W)	
	1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
	1135.7100	1135.6111	87.0474	348	357	(R)QFVTATDVVR(G)	
	1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
	1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDER(T)	
	1585.9400	1585.8477	58.1710	597	610	(R)VYALPEDLVEVNPK(M)	
	1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVIDMSCLR(E)	

7 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900 1689.9700

The matched peptides cover 16% (104/627 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 746520

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FIG. 14C

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely.

Sample ID (comment): Apo A-1 1040 AKPVLEDLR

Database searched: NCBI nr.51403

Molecular weight search (1000 - 200000 Da) selects 1421445 entries.

Full pI range: 1432416 entries.

Species search (HUMAN RODENT) selects 224838 entries.

Combined molecular weight, pI and species searches select 222557 entries.

Number of sequences passing through parent mass filter: 4727

MS-Tag search selects 6 entries.

Parent mass: 1287.7700 (+/- 0.2000 Da)

Fragment ions used in search: 175.00, 255.28, 272.30, 301.48, 369.37, 432.69, 542.65, 633.34, 655.97, 742.67, 840.69 (+/- 0.70 Da)

Ion Types Considered: a b B y n h

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)
identity	2		Trypsin	1			

Result Summary

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	<u>8217500</u>	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	<u>4504965</u>	lymphocyte cytosolic protein 1 (L-plastin)
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.28	MUS MUSCULUS	<u>6679385</u>	65-kDa macrophage protein
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	32331.4 / 8.60	MUS MUSCULUS	<u>12843863</u>	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	<u>26326929</u>	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	<u>29840803</u>	unnamed protein product

Detailed Results

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	MS-Digest Index #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	<u>8217500</u>	<u>696262</u>	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	<u>4504965</u>	<u>725402</u>	lymphocyte cytosolic protein 1 (L-plastin)
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.28	MUS MUSCULUS	<u>6679385</u>	<u>746520</u>	65-kDa macrophage protein
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	32331.4 / 8.60	MUS MUSCULUS	<u>12843863</u>	<u>1146923</u>	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	<u>26326929</u>	<u>1174311</u>	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	<u>29840803</u>	<u>372720</u>	unnamed protein product

Fragment-ion (m/z)	175.00	255.28	272.30	301.48	369.37	432.69	542.65	633.34	655.97	742.67	840.69
Ion-type	y ₁	y ₂ -NH ₃	y ₂	b ₂	y ₃ -NH ₃	b ₃	y ₃	b ₅	y ₆	y ₇	
Delta Da	-0.12	0.13	0.13	0.35	0.18	0.52	0.34	0.09	0.58	0.25	

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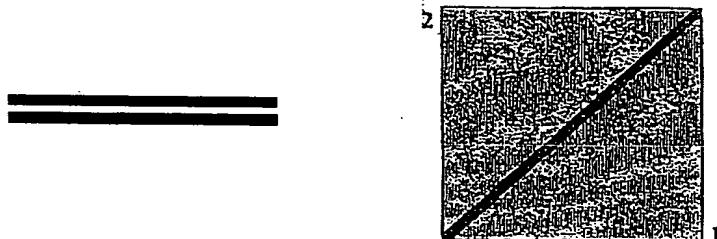
FIG. 15A

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.00 wordsize: 3 Filter 

Sequence 1 gi_72220 heat shock protein 86 - mouse Length 733 (1 .. 733)

Sequence 2 gi_72223 heat shock protein 84 - mouse Length 724 (1 .. 724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1102 bits (2851), Expect = 0.0
 Identities = 564/733 (76%). Positives = 611/733 (82%), Gaps = 9/733 (1%)

Query: 1 MPEETQTQDQPMEEEVE~~T~~FAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIR 60
 Sbjct: 1 MPEEVHHG----EEEVE~~T~~FAFQAEIAQLMSLIINTFYSNKEIFLRELISN+SDALDKIR 55

Query: 61 YESLTDPSKLDGKELHINLIPSQDR~~TLT~~IVDTGIGMTKADLINNLG~~T~~IAKSGTKAFME 120
 Sbjct: 56 YESLTDPSKLDGKELKIDIIPNPQERT~~TLT~~LVDTGIGMTKADLINNLG~~T~~IAKSGTKAFME 115

Query: 121 ALQAGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVR~~TD~~GEPM 180
 Sbjct: 116 ALQAGADISMIGQFGVGFYSAYLVAEKV VITKHNDDEQYAWESSAGGSFTVR D GEP+ 175

Query: 181 GRGTVILHLKEDQTEY~~LE~~ERRRIKEIVKKHSQFIGYPITL~~F~~VEK~~E~~RXXXXXX 240
 Sbjct: 176 GRGTVILHLKEDQTEY~~LE~~ERRVKEVVKKHSQFIGYPITL++E~~K~~E 235

Query: 241 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLNKTKPIWTR 300
 Sbjct: 236 EKEEEDEE~~K~~PKIE~~D~~VGSDEEDDSGKD~~KKKK~~TKK~~I~~KE~~K~~YIDQEE---LNKTKPIWTR 291

Query: 301 NPDDITN~~EE~~YGEFYKSLTN~~D~~WEELAVKHF~~S~~VEGQ~~L~~EFRALLF~~V~~P~~R~~R~~A~~PFDL~~F~~ENRKKKN 360
 Sbjct: 292 NPDDITQ~~EE~~YGEFYKSLTN~~D~~WEELAVKHF~~S~~VEGQ~~L~~EFRALLF~~V~~P~~R~~R~~A~~PFDL~~F~~ENK~~KK~~KN 351

Query: 361 NIKLYVRRVFIMDNCEEL~~I~~PEYLN~~F~~IRGVVDSED~~L~~PLN~~I~~SREMLQQSKILK~~V~~R~~K~~N~~L~~V~~K~~ 420

FIG. 15B

sbjct: 352 NIKLYVRRVFIMD+C+ELI LNFIRGVVDSEDLPLNISREMLQQSKILKVI +VKK
 Query: 421 CLELFTELAEDKENYKKFYEQFSKNIKLGIGHEDSQNRKILSELLRYYTSASGDEMVSLLKD 480
 CLELF+ELAEDKENYKKFYEQFSKNIKLGIGHEDSQNRKILSELLRYYTSASGDEMVSLLKD
 sbjct: 412 CLELFSELAEDKENYKKFYEAFSKNLKLGIGHEDSTNRRRLSELLRYHTSQSGDEMITSLSE 471
 Query: 481 YCTRMKENQKHIYFITGETKQDQVANSASFVERLRKHLCEVIYMIIEPIDEYCVQQLKEFEGK 540
 Y +RMKE QK IX+ITGE+K+QVANSAFVER+RK G EV+YM EPIDEYCVQQLKEF+GK
 sbjct: 472 YVSRMKETQKSIYYITGESKEQVANSASFVERVRKRGFEVVMTEPIDEYCVQQLKEFDGK 531
 Query: 541 TLVSVTXXXXXXXXXXXXXXXXXXXXXXXXXXXXNLCKIMKDILEKKVEKVVVSNRLVTSPCCI 600
 +LVSVT NLCK+MK+IL+KKVEKV +SNRLV+SPCCI
 sbjct: 532 SLVSVTKEGLELPEDEEEKKKMEESKAKPENLCKLMKEILDKKVEKVTISNRLVSSPCCI 591
 Query: 601 VTSTYGTANMERIMKAQALRDNSTMGYMAAKKHLLEINPDHSIIETLRQKAEDKNDKSV 660
 VTSTYGTANMERIMKAQALRDNSTMGYMAAKKHLLEINPDHSIIETLRQKAEDKNDKSV
 sbjct: 592 VTSTYGTANMERIMKAQALRDNSTMGYMAAKKHLLEINPDHPIVETLRQKAEDKNDKAV 651
 Query: 661 KDLVILLYETALLSSGSLEDPQTHANRIYRMIKLGLGIDEDDPVDDTSAAVTEEMPL 720
 KDLV+LL+ETALLSSGSLEDPQTH+NRIFYRMIKLGLGIDED+T++SAAV+E+PPL
 sbjct: 652 KDLVVLFFETALLSSGSLEDPQTHSNRIYRMIKLGLGIDEDDEVTAEEPSAAVPDEIPPL 711
 Query: 721 EGDDDDTSRMEEVD 733
 SGD+D SRMEEVD
 sbjct: 712 EGDEDASRMEEVD 724

CPU time: 0.17 user secs. 0.01 sys. secs 0.18 total secs.

Lambda	K	H
0.316	0.134	0.372

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 5349
 Number of Sequences: 0
 Number of extensions: 384
 Number of successful extensions: 3
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 733
 length of database: 405,742,523
 effective HSP length: 134
 effective length of query: 599
 effective length of database: 405,742,389
 effective search space: 243039691011
 effective search space used: 243039691011
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)

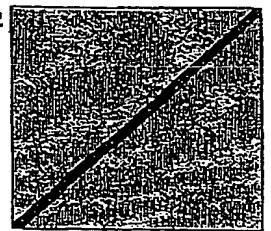
S1: 41 (21.6 bits)
 S2: 78 (34.7 bits)

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FIG. 16A

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.00 wordsize: 3 Filter Aliqots

Sequence 1 gi 72220 heat shock protein 86 - mouse Length 733 (1 .. 733)
 Sequence 2 gi 72223 heat shock protein 84 - mouse Length 724 (1 .. 724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1102 bits (2851), Expect = 0.0
 Identities = 564/733 (76%), Positives = 611/733 (82%), Gaps = 9/733 (1%)

Query: 1 MPEETQTQDQPMEEEEEEVTFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSDALDKIR 60
 MPEE EEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSDALDKIR
 Sbjct: 1 MPEEVHHG----EEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSDALDKIR 55

Query: 61 YESLTDP SKLDSGKELHINLIPSKQDRTLTIVDTGIGMTKADLINNLGTTI AKSGTKAFME 120
 YESLTDP SKLDSGKEL I++IP+ Q+RTLT+VDTGIGMTKADLINNLGTTI AKSGTKAFME
 Sbjct: 56 YESLTDP SKLDSGKELKIDIIIPNPQERTTLTVDTGIGMTKADLINNLGTTI AKSGTKAFME 115

Query: 121 ALQAGADISMIGQFGVGFYSAYLVAEKVTIVTKHNDDEQYAWESSAGGSFTVRLDTGEPM 180
 ALQAGADISMIGQFGVGFYSAYLVAEKV VITKHNDDEQYAWESSAGGSFTVRLDTGEPM
 Sbjct: 116 ALQAGADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRLDTGEPM 175

Query: 181 GRGTVKVLHLKEDQTEYLEERRRIKEIVKKHSQFIGYPITLVEKERXXXXXXXXXXXX 240
 GRGTVKVLHLKEDQTEYLEERRRIKE+VICKHSQFIGYPITL++EKER
 Sbjct: 176 GRGTVKVLHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKEREKEISDDEAEEEKG 235

Query: 241 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLNKTKPIWTR 300
 Sbjct: 236 EKEEEEDKEDEEKPKIEDVGSDEEDDSGKDXXXXTKKIKEKYIDQEE---LNKTKPIWTR 291

Query: 301 NPDDITNEEYGEFYKSLTNDWEHHLAVKHF SVEGQLEPRALLFVPRRAPFDL FENRKKKN 360
 NPDDIT E EYGEFYKSLTNDWE+HLAVKHF SVEGQLEPRALLF+PRRAPFDL P+ENRKKKN
 Sbjct: 292 NPDDITQEYGEFYKSLTNDWEHLAVKHF SVEGQLEPRALLFIPRRRAPFDL FENRKKKN 351

Query: 361 NIKLYVRRVFIMDNCEELIPEYLN FIRGVVDS E DPLN ISREMLQQSKILK VIRK NLVKK 420

FIG. 16B

NIKLYVRRVFIMD+C+EL, LNFIRGVVDSEDLPLNISREMLOQSILKVI AVKK
 Sbjct: 352 NTKLYVRRVFIMDSCDELIBETYLNFTRGVVOSEDPLPNISREMLOQSILKVI, NIVKK 411
 Query: 421 CLELFTELAEDKENYKKFYBQPSKNIKLGIBEDSQNRKELSELLRYYTSASGDEMVSXND 480
 CLELF+ELAEDKENYKKFYE FSIN+KLGIBEDS NR++SELLRY+TS SGDEM SL +
 Sbjct: 412 CLELPSELAEDKENYKKFYEAPSQNLKLGIBEDSTNRBPLSELLRYHTSQSODENTSLSSE 471
 Query: 481 YCTRMKENDQKHYIFITGETKDQVANSAPVERLRRHCLEVYPMIEPIDEYCVQQLKEFEGK 540
 Y+MMKE OK IX+ITGE+K+GVANSAPVER-RK G+EV+YM EPIDSYCVQQLKEFICK
 Sbjct: 472 YVSEKKEKOKSISITVITGESKEQVKAFAVERVYRERGFEVWYHTFIDEYCVQQLKEFQGK 531
 Query: 541 TLVSVTXXXXXXXXXXXXXXXXXXXXXXCRKHOQILEKKVEKVVSNRLVTSPPCI 600
 +LVSAT NLCR+MK+IL+XVERV +SNRLV+SPCCI
 Sbjct: 532 SLVSVTKEGLELPEDEEEKKMEESKAKFENLCKLMKEILDKKEVKVTISNRLLVSSPPCI 591
 Query: 601 VTSTYGTAMMERIMKAQRLRDNTSTMGYMAKQGLBENPDHSIETLRLQKAERDQNDKSV 660
 VTSTYGTAMMERIMKAQRLRDNTSTMGYMAKQGLBENPDHSIETLRLQKAERDQNDKSV
 Sbjct: 592 VTSTYGTAMMERIMKAQABRDNTSTMGYMAKQGLBENPDHSIETLRLQKAERDQNDKAV 651
 Query: 661 KDLVILLYETALLSSGFSLEDPQTHANRIFYRMILGLGIDEDDDPTVDDTSAAUTEMPPL 720
 KDLV+LL+ETALLSSGFSLEDPQTH+NRIFYRMILGLGIDED+ T ++ SAAV +E+PPL
 Sbjct: 652 KDLVLLFETALLSSGFSLEDPQTHSNRIYRMILGLGIDEDDEVTAEEPSAAVPDEIPPL 711
 Query: 721 EGDDDTSRMEEVD 731
 EGDD+O SRMEEVD
 Sbjct: 712 EGDEDASRMEEVD 724

 CPU time: 0.17 user secs. 0.01 sys. secs 0.18 total secs.
 Lambda K H
 0.316 0.134 0.372

 Gapped
 Lambda K H
 0.267 0.0410 0.140

 Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DS: 5349
 Number of Sequences: 0
 Number of extensions: 384
 Number of successful extensions: 3
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 731
 length of database: 405,742,523
 effective HSP length: 134
 effective length of query: 559
 effective length of database: 405,742,389
 effective search space: 243039691011
 effective search space used: 243039691011
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 78 (34.7 bits)